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REVIEW

Effect of Consumption of Animal Products on the Gut Microbiome Composition and Gut Health

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Abstract The gut microbiome is critical in human health, and various dietary factors influence its composition and function. Among these factors, animal products, such as meat, dairy, and eggs, represent crucial sources of essential nutrients for the gut microbiome. However, the correlation and characteristics of livestock consumption with the gut microbiome remain poorly understood. This review aimed to delineate the distinct effects of meat, dairy, and egg products on gut microbiome composition and function. Based on the previous reports, the impact of red meat, white meat, and processed meat consumption on the gut microbiome differs from that of milk, yogurt, cheese, or egg products. In particular, we have focused on animal-originated proteins, a significant nutrient in each livestock product, and revealed that the major proteins in each food elicit diverse effects on the gut microbiome. Collectively, this review highlights the need for further insights into the interactions and mechanisms underlying the impact of animal products on the gut microbiome. A deeper understanding of these interactions would be beneficial in elucidating the development of dietary interventions to prevent and treat diseases linked to the gut microbiome.

Keywords animal products, gut microbiome, meat, dairy products, egg products

Introduction

The gut microbiome is a complex ecosystem comprising trillions of microorganisms that play a crucial role in human and animal health (Bäckhed et al., 2012; Lee et al., 2022; Oh et al., 2021). Diet is a modulator of the gut microbiome, and animal products cause changes in gut microbiome composition and function.

Animal products, such as meat, dairy, and eggs, are excellent sources of protein, vitamins, and minerals, all of which are essential or beneficial for human health (Hess et al., 2016; Puglisi and Fernandez, 2022; Udenigwe and Aluko, 2012; Wyness, 2016).

Animal products contain higher essential amino acid levels than plant proteins (Day et al., 2022). These essential amino acids are derived from animal products and can be metabolized by gut bacteria to produce branched-chain amino acids that are important for the risk of type 2 diabetes (Gojda and Cahova, 2021; Madsen et al., 2017). Menaquinone (MK) is known to help stop and reverse bone loss and is contained mainly in the form of MK-4 in meat, eggs, and dairy products (Walther et al., 2013).

Meat is a prominent source of high-quality protein and essential nutrients such as iron, zinc, and vitamin B12 (Ahmad et al., 2018). Some studies have demonstrated that moderate meat consumption and its proteins compensate for iron deficiency and positively affect the gut microbiome, such as a high abundance of *Lactobacillus* (Krebs et al., 2013; Zhu et al., 2015).

Dairy products refer to foods made from the milk of mammals, such as cows, goats, and sheep, and can include milk, cheese, yogurt, butter, and cream. Dairy products have long been recognized as essential for a healthy and balanced diet because they are high in casein, calcium, and vitamins (Ortega et al., 2019). Nowadays, research has been conducted on the addition of other substances, such as feeding probiotic culture fluids to cows or adding flaxseed to their feed, to improve milk yield or quality (Ababakri et al., 2021; Lim et al., 2021). Consumption of dairy products reduces cardiometabolic risk factors in diet-induced obese mice (Perazza et al., 2020). These dairy products, such as milk, cheese, yogurt, and kefir, contain probiotics that can improve gut health by increasing the abundance of beneficial bacteria such as *Bifidobacterium pseudolongum* and *Lactococcus lactis* (Aslam et al., 2020; Farag et al., 2020; Zhao et al., 2019a).

Eggs and egg products are nutrient-dense food containing various proteins, essential amino acids, vitamins, and minerals, such as vitamin D, vitamin B12, choline, and selenium. These nutrients play an important role in supporting homeostasis in the body, such as brain and nervous system function, metabolism, and immune function (Eckert et al., 2013). In addition, eggs and egg products contain nutrients and bioactive compounds, such as vitamin D and phospholipids, which improve gut health by reducing inflammation (Puglisi and Fernandez, 2022).

Moreover, eggs and egg products have been shown to increase gut microbial metabolites that help maintain a healthy gut lining, such as butyrate and propionic acid. The high protein content in eggs provides a source of essential amino acids for the growth and maintenance of beneficial bacteria in the gut (Ge et al., 2021; Liu et al., 2022a).

Notably, the effects of animal products on the gut microbiome are complex and may depend on the type of animal product and the individual's gut microbiome composition. However, studies summarizing the effects of animal products and proteins on the gut microbiome are limited. In this review, we discussed the effects of meat, dairy, and eggs, which are major animal products, and their processed products on gut microbiome composition and function. Furthermore, the effect of proteins, a major nutritional component of animal products, on the gut microbiome was summarized. Human studies were mainly summarized in this review, and the parts lacking in human studies were reviewed based on animal studies.

Effects of Meat Products and Meat Protein on the Gut Microbiota

Meat products

The gut microbiome is significantly influenced by diet. In particular, meat product consumption affected gut microbiota composition (Table 1). Animal-based diets affect gut microbiota differently than plant-based diets (Muegge et al., 2011; Walker et al., 2011; Wu et al., 2011). Depending on the type of diet, the gut microbiota can change even in a short time, such as 3 days. There was no change in alpha-diversity for either animal- or plant-based diet, but the animal-based diet significantly improved beta-diversity (David et al., 2014). Another study found no significant differences in either the alpha-

Table 1. Human and animal studies assessing the effect of meat product consumption on the composition of gut microbiota

Citation	Study design	Intervention	Trial duration	Participants	Effect on the gut microbiota
Kohnert et al. (2021)	Randomized, controlled trial	Meat-rich diet; >150 g of meat/d Strict vegan diet	4 wk	53 Healthy adults 18–60 yr	In meat-rich group No change in alpha- or beta-diversity *Coprococcus* ↓ *Roseburia* ↑ *Faecalibacterium* ↑ *Blautia* ↑
Russell et al. (2011)	Randomized, crossover trial	Maintenance diet (M); 13% protein and 50% carbohydrates High-protein and moderate-carbohydrate diet (HPMC); 28% protein and 35% carbohydrate High-protein and low-carbohydrate (HPLC); 29% protein and 5% carbohydrate	4 wk	17 Healthy males 21–74 yr Body mass index (BMI) 27.88–48.48	In HPLC group *Roseburia/Eubacterium rectale* ↓ *Bacteroides* spp. ↓
Foerster et al. (2014)	Randomized, crossover trial	Low-meat high-fiber period; whole grain products, 40 g of fiber/d High-meat low-fiber period; 200 g of red meat/d	3 wk	20 Healthy adults 20–60 yr	In high-meat low-fiber period *Clostridium* sp. ↓
Hentges et al. (1977)	Crossover trial	High-beef diet; 380 g of beef/d Meatless diet; 360 g milk; 150 g egg; 145 g cheese; 100 g peas	4 wk	10 Healthy males	In high-beef diet Genus *Bacteroides* ↑ Species *Bacteroides fragilis* ↑ *Bifidobacterium adolescentis* ↓
Zhao et al. (2019b)	Crossover, controlled trial	Beef-based diet Chicken-based diet	2 wk	45 Healthy males 18–27 yr	In beef-based diet *Lachnospira* ↓ *Lachnospiraceae* NK4A136 group ↓ *Ruminococcus* 2 ↓
Dhakal et al. (2022)	Randomized, crossover, controlled trial	Pork group; 156 g pork/d Chicken group; 156 g chicken/d	10 d	50 Healthy older adults 66.44±7.44 yr BMI 29.8±5.59	In both groups No change in alpha- or beta-diversity Phylum *Bacteriodetes* ↓ Family *Bacteriodaceae* ↓ *Christencellaceae* ↑ In pork group *Ruminiclostridium* 5 ↑ In chicken group *Roseburia* ↓

Table 1. Human and animal studies assessing the effect of meat product consumption on the composition of gut microbiota (continued)

Citation	Study design	Intervention	Trial duration	Participants	Effect on the gut microbiota
Shi et al. (2021)	Cross-sectional study	Not applicable (NA)	NA	40 Healthy males 18–30 yr; chicken-eaters (n=20) and pork-eaters (n=20)	In pork-eater group Chao and Shannon index ↓ Phylum *Firmicutes* ↑ *Bacteroidetes* ↓ Genus *Clostridiales, Bacteroides, Firmicutes, Lachnospiraceae, Faecalibacterium, Roseburia, Ruminococcus* 2, and *Blautia* ↑ In chicken-eater group Phylum *Firmicutes* ↓ *Bacteroidetes* ↑ Genus *Prevotellaceae, Prevotella* 9, *Bacteroidales, Dialister, Prevotell*a 2, *Ruminococcaceae* UCG 002, *Lactobacillus*, and *Olsenella* ↑
Sinha et al. (2021)	Dietary intervention (participants were blinded to which group they were assigned)	First phase (2 wk): conventional processed meats (Diet A) Second phase (2 wk): poultry (i.e., chicken and turkey) (Diet B) Third phase (2 wk): Group 1) conventional processed meat supplemented with natural phytochemical compounds (Diet C) Group 2) low-nitrite processed meat supplemented with phytochemical compounds (Diet D) Final phase (1 wk): nitrate-enriched water with diet A, B, C, or D	7 wk	63 Healthy volunteers (participants of each sex were randomly assigned to one of the two experimental groups) (ages 18–70, in good health, with a BMI between 18 and 25 kg/m^2)	NA
Gao et al. (2021)	Randomized controlled-feeding trial	Control group: restricted from fried meat intake (n=58) Fried meat group: fried meat four times per week (n=59)	4 wk	117 Participants, (18–35 yr old, BMI>24 kg/m^2, and consumption of fried food more than one time per wk)	Family *Lachnospiraceae* ↓ Genus *Flavonifractor* ↓ *Dialister* ↑ *Dorea* ↑ *Veillonella* ↑

Table 1. Human and animal studies assessing the effect of meat product consumption on the composition of gut microbiota (continued)

Citation	Control treatment	Experimental treatment	Feeding duration	Animal model	Effect on the gut microbiota
Thøgersen et al. (2018)	Chow, Conventional frankfurter sausage	Inulin-enriched frankfurter sausage	4 wk	30 Healthy Sprague-Dawley rats	Phylum *Actinobacteria* ↑ Family unclassified *Lachnospiraceae* ↑ *Erysipelotrichaceae* ↑ Genus *Bifidobacterium* ↑ Species *Bacteroides uniformis* ↑
Thøgersen et al. (2020)	Control sausage	Sausage+inulin and calcium Sausage+inulin Sausage+calcium	4 wk	48 Healthy Sprague-Dawley rats	Phylum *Firmicutes* ↑ (Sausage+calcium, Sausage+inulin and calcium) *Bacteroidetes* ↓ (Sausage+calcium, Sausage+inulin and calcium) *Proteobacteria*, *Cyanobacteria* ↓ (Sausage+inulin and calcium) *Deferribacteres* ↑ (Sausage+calcium) *Actinobacteria* ↑ (Sausage+inulin and calcium) Genus *Muribaculaceae*, uncultivated *Ruminococcaceae* ↑ (Sausage+Inulin) *Clostridium* 6, *Staphylococcus*, uncultivated *Ruminococcaceae* (PAC000661) ↑ (Sausage+calcium) uncultivated genus (PAC002482), *Parabacteroides*, *Alistipes*, *Clostridium*, unclassified *Peptostreptococcaceae* ↓ (Sausage+calcium) *Bifidobacterium*, *Staphylococcus*, *Blautia*, uncultivated *Ruminococcaceae* (PAC000661), uncultivated *Erysipelotrichaceae* (CCMM), *Faecalibaculum* ↑ (Sausage+inulin and calcium) *Bacteroides*, *Parabacteroides*, *Alistipes*, *Clostridium*, *Dorea*, uncultivated *Bacteroidetes* (PAC002482), *Muribaculaceae* (PAC001472), *Lachnospiraceae* (KE159600), unclassified *Firmicutes* ↓ (Sausage+inulin and calcium) *Lactobacillus* ↑ (q=0.63; Sausage+calcium, Sausage+inulin and calcium)

Table 1. Human and animal studies assessing the effect of meat product consumption on the composition of gut microbiota (continued)

Citation	Control treatment	Experimental treatment	Feeding duration	Animal model	Effect on the gut microbiota
Fernandez et al. (2020)	Control diet (universal feed)	Acorn-fed Iberian commercial ham	2 wk	20 Male Fischer 344 rats (5 wk old) (ulcerative colitis was induced with dextran sulfate sodium in drinking water *ad libitum* for 1 wk)	Phylum *Bacteroidetes, Actinobacteria, Proteobacteria* ↑ *Firmicutes, Synergistetes, Deferribacteres* ↓ Family *Coriobacteriaceae, Bacteroidaceae, Porphyromonadaceae, Rikenellaceae, Desulfovibrionaceae, Sutterellaceae, Staphylococcaceae, Enterococcaceae, Clostridiaceae* Family XIII, *Eubacteriaceae, Acidaminococcaceae, Erysipelotrichaceae, Enterobacteriaceae* ↑ *Marinifilaceae, Prevotellaceae, Sphingobacteriaceae, Ruminococcaceae, Lachnospiraceae, Clostridiaceae, Veillonellaceae, Lactobacillaceae, Cohaesibacteriaceae* ↓ Genus *Bacteroides, Butyricimonas, Parabacteroides, Alistipes, Staphylococcus, Enterococcus, Blautia, Dorea, Absiella, Phascolarctobacterium, Parasutterella, Bilophila* ↑ *Prevotella, Mucispirillum, Lactobacillus, Clostridium, Lachnoanaerobaculum, Ruminococcus, Oscillibacter, Desulfovibrio* ↓

or beta-diversity of the gut microbiota between the animal- and plant-based diets, but did affect the composition of the gut microbiota (Kohnert et al., 2021). The meat-rich diet increased *Roseburia*, *Faecalibacterium,* and *Blautia* more than the strict vegan diet (Kohnert et al., 2021). High animal protein intake and low carbohydrates also affected the reduction of *Bacteroides* spp. while reducing the abundance of the butyrate producer *Roseburia*/*Eubacterium rectale* (Russell et al., 2011).

Meat is a major component of an animal-based diet. Meat is classified as follows: red meat (beef and pork), white meat (chicken and fish), and processed meat. Recent epidemiological studies have reported higher mortality risks and certain chronic diseases in groups that consume more red and processed meat (Al-Shaar et al., 2020; Petermann-Rocha et al., 2021). Moreover, the WHO classified red meat as group 2A, a probable carcinogen (Bouvard et al., 2015). In a review of more than 800 epidemiological studies, >10 studies found a 17% increased risk of colorectal cancer (CRC) for every 100 g increase in red meat intake. Nevertheless, research on the effect of meat product consumption on the gut microbiome remains unclear, and evidence on the effect on health is insufficient.

Consumption of red meat affects the gut microbiome. Consuming 200 g of red meat daily significantly reduced *Clostridium* sp. (Foerster et al., 2014). However, findings on the health effect of *Clostridium* sp. are inconsistent because the changes that occur at the species level are very distinct. In addition, consuming 380 g of beef for 4 weeks affected the reduction of diarrheal disease-related *Bacteroides fragilis* and the increase of intestinal movement regulator *Bifidobacterium adolescentis* (Hentges et al., 1977). Meanwhile, there are studies comparing the effects of red and white meat consumption on the gut microbiome. A beef-based diet increased the relative abundance of *Lachnospira*, the *Lachnospiraceae* NK4A136 group, and *Ruminococcus* 2, whereas the chicken-based diet did not show significant changes (Zhao et al., 2022). After consuming a beef-based diet, *Akkermansia muciniphila* was reduced and blood cell counts were elevated, altering markers associated with inflammation. Replacing the beef-based diet with a chicken-based diet reduced inflammation-related monocytes and basophils. This appears to be related to the chicken-based diet's suppression of *Bacteroides ovatus*, a factor in generating immunoglobulin A. In an intervention study in which pork or chicken was consumed, both groups altered the gut microbiota in a similar pattern, with reductions in the *Bacteroidetes* phylum, *Bacteroidaceae*, and *Christencellaceae* families (Dhakal et al., 2022). However, in a cross-sectional study observing pork and chicken eaters, high *Bacteroidetes* levels were found in the chicken eaters, and differences were observed at the species level (Shi et al., 2021).

It is well-recognized that meat consumption is harmful to persons with diseases. Red meat may increase the gut microbiota's production of uremic toxins such as trimethylamine (TMA) n-oxide (TMAO), indoxyl sulfate, and p-cresyl sulfate. These uremic toxins are linked to a higher risk of cardiovascular death (Mafra et al., 2018). In addition, red meat, unlike white meat, is associated with CRC (Sasso and Latella, 2018). This is mainly because of the red-colored heme iron found in large quantities in the muscle myoglobin of red meat. Heme iron causes direct harm, such as causing cytotoxic damage to colonic epithelial cells, and indirect harm by inducing alterations of the gut microbiota (Ijssennagger et al., 2012). A red meat diet rich in heme iron increases *Streptococcus bovis*, *Fusobacterium*, *Clostridium*, and *Helicobacter pylori*, which are related to colorectal carcinogenesis (Sasso and Latella, 2018). However, it is unclear whether the increase or decrease in the gut microbiome caused by certain substances, such as toxins and heme iron, contributes to diseases.

Meanwhile, in inflammatory bowel disease (IBD)-induced mouse experiments, high-dose red meat induced intestinal microbial imbalance and reduced the relative abundances of *Lachnospiraceae*_NK4A136_group, *Faecalibaculum*, *Blautia*, and *Dubosiella* (Li et al., 2021). This results from a study that contradicts the previous healthy human study in which beef intake increased *Lachnospiraceae*_NK4A136_group. *Lachnospiraceae*_NK4A136_group is a butyrate-producing bacteria that protects the intestinal mucosal and reduces inflammation (Li et al., 2021; Zhao et al., 2022).

Taken together, red, white, and processed meats are all observed to have different effects on the gut microbiome. However, there are currently insufficient studies that compile adequate information to determine consistent changes in the gut microbiome. In addition, like other food consumption, excessive meat consumption has also been linked in studies to the emergence of disease, albeit the exact mechanisms related to alterations in the gut microbiome are unknown.

Processed meat products

The WHO classified processed meats as group 1 carcinogens (Bouvard et al., 2015). The consumption of processed meat is known to increase the incidence of CRC. N-nitroso compounds, such as nitrates used as preservatives in processed meat, are considered the leading cause of CRC. Moreover, certain microorganisms in the gut can reduce nitrate to nitrite through metabolic processes (González-Soltero et al., 2020). However, a diet containing processed meat and an intake of nitrate-rich water did not show significant changes in the fecal microbiome (Sinha et al., 2021).

One human study confirmed the correlation between fried meat intake and gut microbiota. A randomized controlled trial was conducted for 4 weeks, and the gut microbiota of 59 participants in the group treated with fried meat and 58 participants in the control group with restricted fried meat intake were compared. In the gut microbiome of the fried meat intake group, *Lachnospiraceae* and *Flavonifractor* decreased, and *Dialister, Dorea,* and *Veillonella* increased (Gao et al., 2021).

There are two studies in rats on the correlation between consuming sausage and the modulation of gut microbiota. In one study, rats were fed for 4 weeks on one of three diets: inulin-fortified pork sausage, control pork sausage, or standard chow diet. Rats in the inulin-fortified pork sausage group had increased abundances of *Actinobacteria,* unclassified *Lachnospiraceae, Erysipelotrichaceae, Bifidobacterium*, and *Bacteroides uniformis*. In addition, unlike conventional sausages, the sausage fortified with inulin showed similar effects to the general dietary fiber intake, such as increasing short-chain fatty acid (SCFA) and *Bifidobacteria* (Thøgersen et al., 2018). In a subsequent study, rats were fed for 4 weeks on one of four diets: control sausage, sausage with added inulin and calcium, sausage with added inulin, and sausage with added calcium. In the gut microbiota of the two groups of rats fed the calcium-rich sausage and calcium-added inulin-fortified sausage, *Firmicutes* increased, and *Bacteroidetes* decreased at the phylum level. At the genus level, *Ruminococcaceae* and *Staphylococcus* were increased in both groups, and in particular, *Bifidobacteria* were increased in the intestinal microflora of rats in the group fed sausages calcium-rich and fortified with inulin (Thøgersen et al., 2020).

Acorn-fed Iberian ham is a traditional cured meat product. A study was conducted on changes in gut microbiota caused by an acorn-fed ham diet using rats as an experimental model. The acorn-fed ham diet had a lower carbohydrate content and higher protein content than that of the control diet, resulting in increased proteolytic metabolism-related *Bacteroidetes* and *Proteobacteria* and decreased saccharolytic metabolism-related *Firmicutes* at the phylum level. In addition, *Dorea*, *Phascolarctobacterium*, or *Butyricimonas*, which are highly related to ulcerative colitis disease, were decreased at the genus level (Fernández et al., 2020).

In conclusion, consumption of different types of processed meats can cause changes in the gut microbiome. However, processed meat consumption was not associated with adverse changes in the gut microbiome, such as an increase in pathogenic bacteria or dysbiosis. These results show that there is no clear causal link between processed meat consumption and adverse health effects of changes in the gut microbiome.

Meat protein

Proteins can show different changes in the composition of the intestinal microbiota depending on the type, such as plant and animal origin. Animal food-originated protein is a great source of nutrients and can affect the composition of the gut microbiome (Lang et al., 2018). However, no human study has directly tested the effect of meat protein intake on the modulation of the gut microbiome; however, there have been animal studies.

In one study using a rat model, the effect of various dietary proteins, such as plant (soy), dairy (casein), red meat (beef and pork), and white meat (chicken and fish) proteins, on the composition of gut microbiota was assessed (Zhu et al., 2015). At the phylum level, the group fed white meat protein had a higher abundance of *Firmicutes* but lower *Bacteroidetes* than the other groups. Conversely, the chicken protein-fed group had a higher abundance of *Actinobacteria*, and the rats fed beef protein had a higher abundance of *Proteobacteria*. At the genus level, *Ruminococcaceae* and *Lactobacillaceae* were abundant in the group fed red meat protein, and *Lactobacillaceae* were more abundant in the group fed white meat protein. Consumption of meat protein reduced serum lipopolysaccharide-binding protein (LBP) compared to soy protein. Typically, the presence of LBP in the blood is regarded as a biomarker of an inflammatory reaction. This may be related to the

composition of the gut microbiome. *Bacteroidetes* are major lipopolysaccharide (LPS)-producing bacteria, which are reduced by consuming meat proteins. Therefore, casein and meat protein intake may help maintain gut microbiome balance and reduce antigen load and inflammatory response. In addition, when comparing each group, meat proteins, mainly white meat proteins, contained more *Lactobacillus* than non-meat proteins (casein, soy). *Lactobacillus* is well known as representative probiotic bacteria. In other words, the recommended level of meat protein intake could help the growth of beneficial intestinal bacteria such as *Lactobacillus* (Zhu et al., 2015).

White meat-originated protein consumption has been linked to alterations in the gut microbiome in two rat model studies. Zhu et al. compared the feces of 4-week-old and 64-week-old rats fed a chicken protein diet. The results showed that the gut microbiome composition differed significantly between young and middle-aged mice. At the phylum level, *Firmicutes* decreased for middle-aged rats but increased for young rats. However, the level of *Bacteroidetes* increased for middle-aged rats and decreased for young rats. At the genus level, the relative abundance of the beneficial bacterium *Lactobacillus* increased by chicken protein in the young group. In contrast, it had the opposite effect in the middle-aged group (Zhu et al., 2016a). In another study, the relative abundance of *Lactobacillus* was higher in the chicken protein group than in the casein control group; it also showed the highest levels of organic acids, including lactate, which can promote the growth of *Lactobacillus* (Zhu et al., 2017).

A. muciniphila is considered a next-generation probiotic bacteria (Ross, 2022). It plays significant roles in lipid metabolism and enhances intestinal immune function to prevent obesity, IBD, and diabetes (Rodrigues et al., 2022). In a study that compared the effects of soy and chicken protein-based diet intake on the composition of intestinal microbiota using a germ-free mice model, compared to a soy protein-based diet, a chicken protein-based diet helped the growth of *A. muciniphila* and maintained mucus barrier function and intestinal homeostasis (Zhao et al., 2019b).

Overall, red meat proteins can modulate the alteration of the gut microbiome in a direction that reduces LPS-producing bacteria. White meat protein may help maintain gut homeostasis by increasing *Lactobacillus* or *A. muciniphila* levels. However, numerous perspectives on the gut microbiota of meat protein consumption have been reported in prior research. Therefore, more research is required to provide clear scientific evidence.

Effects of Dairy Products and Dairy Protein on the Gut Microbiota

Dairy products

Investigations have examined how dairy products, including milk, yogurt, and cheese, affect the gut microbiome (Table 2). Two studies reported the effects of the quantity of dairy products on the gut microbiota. Swarte et al. (2020) divided 46 healthy overweight adults into high-dairy diet (HDD) and a low-dairy diet (LDD) groups for 6 weeks. HDD showed relatively higher *Streptococcus, Leuconostoc*, and *Lactococcus* abundances and lower *Faecalibacterium* and *Bilophila* abundances. At the species level, the abundances of *Streptococcus thermophilus* and *Leuconostoc mesenteroides* were increased; however, *Faecalibacterium prausnitzii* and *Clostridium aldenense* were decreased. Predicted metabolic pathways were also studied; however, there were no significant changes by HDD (Swarte et al., 2020). Alternatively, a randomized controlled trial was performed in one human study for 24 weeks; however, there was no significant change in gut microbiota composition or diversity according to the difference in dairy intake (Bendtsen et al., 2018).

Another human study analyzed the correlation between consuming whole milk and gut microbiota. In the 3-month randomized, double-blind study, 24 of 64 male participants received 500 mL of bovine milk daily. Then, the relative

Table 2. Human and animal studies assessing the effect of dairy product consumption on the composition of gut microbiota

Citation	Study design	Intervention	Trial duration	Participants	Effect on the gut microbiota	Other health or physiological observations
Swarte et al. (2020)	Randomized, cross-over trial	Quantity of dairy High-dairy diet (HDD); 5–6 dairy portion/d Low-dairy diet (LDD); ≤1 dairy portion/d	6 wk	46 Healthy overweight participants 45–65 yr Body mass index (BMI) 25–30	In HDD Genus *Streptococcus, Leuconostoc*, and *Lactococcus* ↑ *Faecalibacterium* and *Bilophila* ↓ Species *Streptococcus thermophilus* ↑ *Erysipelatoclostridium ramosum* ↑ *Leuconostoc mesenteroides* ↑ *Faecalibacterium prausnitzii* ↓ *Clostridium aldenense* ↓ *Acetivibrio ethanolgignens* ↓ *Bilophila wadsworthia* ↓ *Lactococcus lactis* ↓	Predicted metabolic pathways were not significantly altered due to a HDD
Bendtsen et al. (2018)	Randomized, controlled, parallel trial	Quantity of dairy High dairy (HD); 1,500 mg calcium/d Low dairy (LD); 600 mg calcium/d	24 wk	80 Overweight or obese participants 18–60 yr BMI 28–36; 40 consumed HD and 40 consumed LD	No significant taxonomic changes in phylum and genus level No significant changes in alpha- or beta-diversity *Veillonella* ↓ in LD (vs baseline)	In both groups Body weight ↓ (vs baseline) Fat mass ↓ (vs baseline) Respiratory quotient (RQ) ↓ in HD RQ ↑ in LD
Fernandez-Raudales et al. (2012)	Randomized, double blind trial	Bovine milk, 500 mL/d	3 mon	64 Male participants 20–45 yr BMI 25–44; 24 consumed bovine milk	Phylum *Proteobacteria* ↑ Genus *Lactobacillus* ↑ (vs baseline) Alpha-diversity ACE ↓ Chao1 ↓	NA
Alvaro et al. (2007)	Cross-sectional study	Yogurt 200–400 g/d	Not applicable (NA)	51 Healthy participants 35–60 yr; 30 consumed yogurt	*Enterobacteriaceae* ↓ No significant difference in short-chain fatty acid (SCFA) concentration	β-galactosidase ↑
González et al. (2019)	Cross-sectional study	NA	NA	130 Healthy participants mean age of 58.18	Natural yogurt consumers *Akkermansia* ↑ Sweetened yogurt consumers *Bacteroides* ↓ Cheese consumers SCFA (acetate, propionate and butyrate) ↑	Serum levels of C-reactive protein (CRP) were also significantly reduced in yogurt consumers
Le Roy et al. (2022)	Cross-sectional study	Yogurt 125 g at least once a wk	NA	4,117 Adult participants mean age of 67.6 yr	*Bifidobacterium animalis* subsp. *lactis* ↑ *Streptococcus thermophilus* ↑	Visceral fat mass ↓

Table 2. Human and animal studies assessing the effect of dairy product consumption on the composition of gut microbiota (continued)

Citation	Study design	Intervention	Trial duration	Participants	Effect on the gut microbiota	Other health or physiological observations
Tillisch et al. (2013)	Randomized, controlled, parallel trial	Fermented milk 2×125 g/d	4 wk	36 Healthy female participants 18–55 yr; 12 consumed fermented milk	No significant changes in the gut microbiota composition after the intervention	Activity of brain regions that control central processing of emotion and sensation was affected by intervention
Lisko et al. (2017)	Parallel trial	Yogurt 250 g/d	6 wk	6 Healthy participants 18–54 yr	No significant changes in the gut microbiota composition and diversity	NA
Link-Amster et al. (1994)	Randomized, controlled trial	Fermented milk 3×125 g/d	3 wk	30 Healthy adult participants F=14, M=16 19–59 yr; 16 consumed fermented milk	Genus *Lactobacillus* ↑ *Bifidobacterium* ↑ Species *Lactobacillus acidophilus* ↑	Serum IgA and IgG ↑
Volokh et al. (2019)	Before and after trial	Yogurt 2×125 g/d	30 d	150 Healthy adult participants 18–40 yr BMI 18–28	No significant change in alpha-diversity after intervention Genus *Bifidobacterium* ↑ *Lachnoclostridium*/unclassified ↓ *Roseburia* ↓ Species *B. bifidum, B. adolescentis, B. animalis, B. bifidum, B. longum* ↑ *Adlercreutzia equolifaciens* ↑ *Slackia isoflavoniconvertens* ↑ *Collinsella aerofaciens* ↑ *Catenibacterium. mitsuokai* ↑ *Streptococcus. thermophilus/vestibularis* ↑	NA
Burton et al. (2017)	Randomized, double-blind, cross-over trial	Yogurt 400 g/d	2 wk	14 Healthy male participants 22–27 yr; 7 consumed yogurt	*Lactobacillus delbrueckii* spp. *bulgaricus* ↑ *Streptococcus salivarius* spp. *thermophilus* ↑	Tumor necrosis factor (TNF)α, interleukin (IL)-6 and C-C motif chemokine ligand 5 (CCL5) ↓ (vs baseline)
Alvarez et al. (2020)	Randomized, double-blind, controlled, parallel trial	Yogurt 100 g/d or 3×100 g/d	4 wk	96 Healthy adult participants 18–55 yr BMI 18.5–30.0; 25 consumed 100 g/d yogurt and 24 consumed 3×100 g/d yogurt	*Lactobacillus paracasei* ↑ *Lactobacillus rhamnosus* ↑ No significant difference in either alpha- or beta-diversity	No clinically significant changes in defecation frequency, stool consistency scores, composite score and frequency of digestive symptoms (abdominal pain, bloating, flatulence and rumbling) or vital signs

Table 2. Human and animal studies assessing the effect of dairy product consumption on the composition of gut microbiota (continued)

Citation	Study design	Intervention	Trial duration	Participants	Effect on the gut microbiota	Other health or physiological observations
García-Albiach et al. (2008)	Randomized, double-blind, cross-over trial	Yogurt 3×125 g/d	2 wk	79 Healthy young participants mean age of 23.6 yr; 32 consumed fresh yogurt	Lactic acid bacteria ↑ *Clostridium perfringens* ↑ *Bacteroides* ↓	NA
Unno et al. (2015)	Before and after trial	Fermented milk 2×140 mL/d	3 wk	6 Healthy female participants 20–24 yr	Phylum *Firmicutes* ↑ *Bacteroidetes* ↓ Alpha-diversity (Shannon index) ↓	NA
Yang and Sheu (2012)	Parallel trial	Yogurt 200 mL/d	4 wk	38 *Helicobacter pylori*-infected and 38 healthy children 4–12 yr	*E. coli* ↓ *Bifidobacterium* spp. ↑ *Bifidobacterium* spp./*E. coli* ratio ↑	In *H. pylori* infected children ^{13}C-Urea breath test ↓ (vs baseline) IgA ↑ IL-6 ↓
Veiga et al. (2014)	Randomized, double blind, controlled, parallel trial	Fermented milk 2×125 g/d	4 wk	28 Female inflammatory bowel disease patients 20–69 yr; 13 consumed fermented milk	*Bilophila wadsworthia* ↓ Butyrate-producing bacteria ↑ SCFA ↑	NA
Yılmaz et al. (2019)	Randomized, controlled, open-label, parallel trial	Kefir 400 mL/d	4 wk	45 Inflammatory bowel disease patients; 10 Crohn disease (CD) patients and 15 ulcerative colitis patients consumed kefir	*Lactobacillus* ↑	In CD erythrocyte sedimentation rate ↓ CRP ↓ hemoglobin ↑ bloating ↓ feeling good scores ↑
Bellikci-Koyu et al. (2019)	Randomized, controlled, parallel trial	Kefir 180 mL/d	12 wk	22 Metabolic syndrome patients 18–65 yr; 12 consumed kefir	*Actinobacteria* ↑ No significant difference in either alpha- or beta-diversity	Fasting insulin, homeostatic model assessment for insulin resistance (HOMA-IR), TNF-α, interferron (IFN)-γ, and systolic and diastolic blood pressure ↓ (vs baseline)
Hric et al. (2021)	Randomized, controlled, parallel trial	Bryndza cheeses 30 g/d	4 wk	22 Female participants 18–65 yr BMI 20–40; 13 consumed Bryndza cheese	No significant change in alpha-diversity within and between the groups. Order *Lactobacillales* ↑ (vs baseline) Family *Streptococcaceae* ↑	NA

Table 2. Human and animal studies assessing the effect of dairy product consumption on the composition of gut microbiota (continued)

Citation	Study design	Intervention	Trial duration	Participants	Effect on the gut microbiota	Other health or physiological observations
					(vs baseline) Genus *Lactococcus* and *Streptococcus* ↑ (vs baseline) *Phascolarctobacterium* and *Butyricimonas* ↑ (vs baseline)	
Milani et al. (2019)	Randomized, controlled, parallel trial	Parmesan cheese 45 g/d	7 d	20 Healthy participants	*Bifidobacterium mongoliense* ↑	NA
Firmesse et al. (2007)	Before and after trial	Camembert cheese 2×40 g/d	4 wk	12 Healthy participants (no age specified)	*Enterococcus faecalis* ↑ (vs baseline)	NA
Firmesse et al. (2008)	Before and after trial	Camembert cheese 2×40 g/d	4 wk	12 Healthy participants 19–40 yr	*Lactococcus lactis* ↑ *Leuconostoc mesenteroides* ↑ No significant changes in bacterial enzyme activities and SCFA concentration	NA

abundance of members in the phylum *Proteobacteria* significantly increased. At the genus level, *Lactobacillus* and *Roseburia* tended to increase, whereas *Prevotella* decreased (Fernandez-Raudales et al., 2012).

There was more research on yogurt intake and gut microbiota change than on other dairy products. First, three cross-sectional studies were identified from each cohort study performed in France, Spain, and the United Kingdom. Thirty healthy adults who consumed at least 200–400 g of yogurt daily had significantly lower *Enterobacteriaceae* levels than those who did not consume yogurt daily. Although there was no difference in the intestinal SCFA concentration between the groups, β-galactosidase activity was significantly increased in the yogurt intake group (Alvaro et al., 2007). In another study, annual dietary fermented food intake was investigated by a food frequency questionnaire (FFQ) from 130 people. Natural yogurt consumers showed significantly higher fecal levels of *Akkermansia,* and sweetened yogurt consumers displayed significantly lower fecal levels of *Bacteroides*. Additionally, cheese consumers presented significantly higher levels of the major fecal SCFAs (acetate, propionate, and butyrate; González et al., 2019). According to another FFQ survey from 4,117 participants, >73% consumed 125 g of yogurt at least once weekly and had higher abundances of *Bifidobacterium animalis* subsp. *Lactis* and *S. thermophilus* (Le Roy et al., 2022).

In a study of 36 healthy adult women who consumed fermented milk for 4 weeks, no significant changes in gut microbiota were found (Tillisch et al., 2013). Similarly, six healthy adults who consumed yogurt for 6 weeks showed no significant changes in gut microbiota composition or diversity (Lisko et al., 2017). However, unlike these two studies, most studies found that consuming fermented dairy products affected gut microbiota, particularly *Lactobacillus* and *Bifidobacterium*. Fermented milk intake was associated with increased intestinal *Lactobacillus* (particularly *Lactobacillus acidophilus*) and *Bifidobacterium* (Link-Amster et al., 1994). It was also confirmed that the intestinal *Bifidobacterium* increased, while *Roseburia* decreased after consuming fermented milk (Volokh et al., 2019). In addition, three randomized, double-blind studies found that yogurt intake affected the increase in intestinal *Lactobacillus* spp. Specifically, consuming 400 g of yogurt

daily for 2 weeks was associated with increased intestinal *Lactobacillus delbrueckii* spp. *bulgaricus* and *Streptococcus salivarius* spp. *thermophiles* (Burton et al., 2017). One study found that yogurt consumption increased *Lactobacillus paracasei* and *Lactobacillus rhamnosus* but did not affect alpha- or beta-diversity (Alvarez et al., 2020). The increased *L. rhamnosus* in this study has been shown to improve the immune response in another study (Kang et al., 2021a). García-Albiach et al. (2008) reported that yogurt consumption increased the intestinal density of lactic acid bacteria (LAB) and the pathogen *Clostridium perfringens* (García-Albiach et al., 2008). Similarly, fermented milk intake increased *Firmicutes* and decreased *Bacteroidetes* at the phylum level (Unno et al., 2015).

Consumption of fermented dairy products also inhibits pathogens in pathological conditions. In 38 *H. pylori*-infected children, when 200 mL of yogurt was consumed daily for 4 weeks, the representative pathogen *Escherichia coli* decreased, and the beneficial bacteria *Bifidobacterium* spp. increased (Yang and Sheu, 2012). Additionally, fermented milk consumption decreased *Bilophila wadsworthia* levels in patients with IBD, which is a strain known to cause IBD by inducing barrier collapse by producing hydrogen sulfide. Meanwhile, the intake of fermented milk increased intestinal SCFA concentration and significantly increased the level of butyrate-producing bacteria. Among SCFAs, butyrate is particularly helpful in strengthening the gut barrier (Veiga et al., 2014). Kefir intake significantly increased the abundance of *Lactobacillus* in the gut microbiota of patients with IBD (Yılmaz et al., 2019). Another study showed that ingestion of kefir increased the relative abundance of *Actinobacteria* but had no significant effect on *Bacteroidetes*, *Proteobacteria*, or *Verrucomicrobia* (Bellikci-Koyu et al., 2019).

Cheese is a high-protein-containing dairy product, a densely nutrient-rich solid food, unlike raw milk or yogurt. Four studies reported the effect of cheese consumption on gut microbiota. When 13 female adults consumed 30 g of Bryndza cheese daily for 4 weeks, there was no change in alpha-diversity; however, the relative abundance of LAB (*Lactobacillales*, *Streptococcaceae*, *Lactococcus*, and *Streptococcus*) significantly increased. Additionally, SCFA producers such as *Phascolarctobacterium* and *Butyricimonas* increased significantly in Bryndza cheese consumers (Hric et al., 2021). A human pilot study of Parmesan cheese consumption for 7 days showed that *Bifidobacterium mongoliense* strains from cheese could transiently colonize the human gut (Milani et al., 2019). In two studies of Camembert cheese intake affecting gut microbiota, higher *Enterococcus faecalis*, *L. lactis*, and *L. mesenteroides* levels were found in fecal samples (Firmesse et al., 2007; Firmesse et al., 2008).

In conclusion, intake and types of dairy products are important gut microbiome-changing factors. A higher dairy product intake increases the intestinal *Lactobacillus* and *Bifidobacterium* levels. In *H. pylori* infection or IBD condition, consuming fermented dairy products may help hosts suppress the pathogen proliferation. Most reported studies have confirmed that consuming dairy products can improve host health by increasing the number of beneficial bacteria in the gut.

Dairy protein

Numerous studies are underway to determine why consuming dairy products alters the gut microbiome. Dairy nutrients have been the subject of several studies (Ha et al., 2021; Lim et al., 2020). It is also used to enhance the quality of other foods (Kang et al., 2021b). Several studies have examined how dairy proteins affect the gut microbiome. The gut microbiome of rats changed according to the intake of milk protein. When 14% or 53% of whole milk protein was fed to rats, there were changes in microbiota composition, such as a decrease in gene copy numbers in *Clostridium coccoides* and *Clostridium leptum* groups in the high protein group compared to that in the normal protein group (Liu et al., 2014). However, studies on casein or whey proteins have been increasing. Casein and whey proteins are known as the main proteins in milk. In particular, casein constitutes approximately 80% of the total protein in milk, while whey protein accounts for approximately 20% (Davoodi et al., 2016).

One study fed casein to mice for 2 weeks. The abundance of *Bacteroidetes* at the phylum level significantly increased in the

casein-treated group, while *Lachnospiraceae* and *Ruminococcaceae* decreased at the family level, and *Parabacteroides* and *Bacteroides* increased at the genus level (Kim et al., 2016). Other studies have also shown that the gut microbiome changes when high casein concentrations are ingested. When the rats were fed diets containing either 19.4% or 52% casein for 24 weeks, the gut microbiota of the groups fed high casein concentrations were altered. At the phylum level, there was a relative expansion of *Actinobacteria* and a relative contraction of *Saccaribacteria*. At the genus level, there was an expansion of *Bifidobacterium*, *Bacteroides*, *Parabacteroides,* and *Oscillospira* (Snelson et al., 2021). Alternatively, another study reported that changes in the gut microbiota caused by a high casein intake could be detrimental to intestinal health. This is because the relative abundance of pathogens in the colon increased in the 54% high-concentration casein intake (HCD) group compared to that in the normal intake (20% casein; NCD) group. *Escherichia*/*Shigella*, *Enterococcus*, *Streptococcus*, and sulfate-reducing bacteria increased >2–5 times in the HCD group compared to the NCD group. In contrast, *Ruminococcus*, *Akkermansia*, and *F. prausnitzii*, which are generally regarded as beneficial bacteria in the large intestine, were reduced (Mu et al., 2016). In another study, the number of *E. coli* increased in the HCD group, whereas bacteria that protect intestinal epithelium (*A. muciniphila*, *Bifidobacterium*), propionate-producing bacteria (*Prevotella*), butyrate-producing bacteria (*Roseburia*/*Eubacterium rectale*), and acetate producing bacteria (*Ruminococcus bromii*), were reduced (Mu et al., 2017). However, studies remain insufficient to suggest that changes in the gut microbiota caused by a high casein intake may be detrimental to gut health.

Conversely, casein is a non-meat protein that changes gut microbiota close to soy protein, and there was no difference in alpha- and beta-diversity between human groups consuming casein or soy protein (Beaumont et al., 2017). In animal experiments, casein intake was similar to the gut bacteria composition of soy protein-treated groups rather than chicken, beef, and fish protein-treated groups. One study showed that casein consumption was related to the relative abundance of *Lachnospiraceae* (Zhu et al., 2016b). Similar to this study, rats fed with soy protein and casein had similar gut bacterial profiles at the family level that was characteristic of *Lachnospiraceae* (Zhu et al., 2015). Members of the *Lachnospiraceae* family are known to protect the gut against human colon cancer by producing butyrate. Additionally, the lower relative abundance of *Lactobacillus* is associated with casein intake (Rist et al., 2014; Zhu et al., 2015; Zhu et al., 2016b).

Whey protein affects gut microbiota composition differently compared to casein. When high-fat diet mice were treated with casein or whey protein, differences in beta-diversity were observed between groups (Boscaini et al., 2019). Another study showed a significantly higher proportion of *Streptococcaceae* at the family level in the group fed a diet containing casein as the primary protein source (Boscaini et al., 2019; Boscaini et al., 2020; Nilaweera et al., 2017). In addition, high proportions of *Lactobacillus* and *Bifidobacterium* were mainly observed in the group that consumed whey protein (Boscaini et al., 2019; Boscaini et al., 2020; Boudry et al., 2013; McAllan et al., 2014; Schaafsma et al., 2021; Sprong et al., 2010). The combination of *Lactobacillus* and *Bifidobacterium* has been mentioned in one study as a potential candidate strain to be used for immune enhancement, thus an increase in the proportion of *Lactobacillus* and *Bifidobacterium* in the gut microbiome could potentially associated with immune enhancing effects (Yu et al., 2022). In two studies by Boscaini et al. comparing casein and whey protein, at the family level, the relative abundance of *Streptococcaceae* was higher in the casein group, and the relative abundance of *Lactobacillaceae* was higher in the whey protein group. At the genus level, the relative abundance of *Lactococcus* was higher in the casein group, and the relative abundances of *Parabacteroides*, *Lactobacillus*, and *Bifidobacterium* were higher in the whey protein group (Boscaini et al., 2019; Boscaini et al., 2020). In a study by Nilaweera et al. (2017) casein intake increased the proportion of *Enterobacteriaceae* and *Streptococcaceae* compared to the whey protein intake group (Nilaweera et al., 2017). Compared to casein, cheese whey protein increased fecal *Lactobacilli* and *Bifidobacteria* counts in a colitis-induced rat model (Sprong et al., 2010), and a lactoperoxidase and lactoferrin-enriched whey protein isolate increased

Lactobacillaceae/*Lactobacillus* and decreased *Clostridiaceae*/*Clostridium* in high-fat diet-fed mice (McAllan et al., 2014). In a human study to examine sleep quality and stress, those on a whey protein-based diet had significantly increased relative abundances of *Bifidobacterium* compared to the casein intake group (Schaafsma et al., 2021). Whey peptide extracts with a molecular weight of <1 kDa increased *Lactobacillus* spp. and *Bifidobacterium* spp. (Boudry et al., 2013).

In conclusion, a long-term high-protein diet causes gut microbiota imbalance and increases intestinal permeability. However, normal levels of casein intake constitute a gut microbiome that regulates the *Lachnospiraceae* family similarly to soy protein. Changes in the gut microbiome by whey protein intake increased beneficial bacteria such as *Lactobacillus* and *Bifidobacterium*, similar to the changes in the intake of dairy products.

Effects of Egg Products and Egg Protein on the Gut Microbiota

Egg products

We summarized previous studies on the impact of egg products and their proteins on the composition and function of the gut microbiome (Table 3). Eggs have different effects on the gut microbiome depending on the species and processing method. There are studies on hen egg white (HEW), duck egg white (DEW), and preserved duck egg white (PEW) using rats as experimental models. *Akkermansia* and *Peptostreptococcaceae* were relatively high in abundance in the HEW and DEW groups, respectively. In the PEW group, the intestinal microbe richness was significantly lower than that of other groups, and in particular, compared to DEW, *Proteobacteria* abundance was relatively low. Egg consumption effects on gut microbes may differ depending on the egg type and processing method (Yu et al., 2020).

In a study comparing the effects of duck eggs and preserved duck egg intake on changes in gut microbial composition using rats as experimental models, the ingestion of preserved duck eggs increased the α-diversity of gut microbes compared to the duck egg group. There was no significant difference at the phylum level; however, *Firmicutes*/*Bacteroidetes* were decreased. At the genus level, *Veillonella*, *Phascolarctobacterium*, *Alpinimonas*, *Coprococcus* 3, *Coprococcus* 2, *Gelria,* and unclassified *Methylocystaceae*, which were not found in the duck egg group, were found (Meng et al., 2020).

Egg yolk is a food ingredient commonly used in various processed foods. A study using the mouse as an experimental model found that *Firmicutes* and *Epsilonbacteraeota* were relatively decreased at the phylum level when egg yolk was fed. In addition, *Lachnospiraceae* and *Ruminococcaceae* were significantly reduced at the family level, and *Erysipelotrichaceae* was significantly increased. At the genus level, *Parasutterella* and *Coprostanoligenes* showed a relatively high abundance (Fukunaga et al., 2020). *Parasutterella* has been defined as a core component of the human and mouse gut microbiota and has been correlated with bile acid maintenance and cholesterol metabolism (Ju et al., 2019). *Coprostanoligenes* is a bacteria that can influence host cholesterol levels. Therefore, these results indicate that egg yolk consumption can induce changes in gut microbiota related to cholesterol metabolism (Kenny et al., 2020).

In a study on the change in gut microbes by comparing the gut microbes of obese and lean rats and treating the obese rats with egg white hydrolyzed with pepsin (EWH), the gut microbe composition of obese and lean rats showed significant differences at the phylum and genus levels. However, in the gut microbiome composition of obese rats fed EWH, *Lactobacillus*/*Enterococcus* and *C. leptum* were similar to those of lean rats. Conversely, the change in the microbial composition observed after ingestion of EWH did not show the final weight loss effect in obese rats. Thus, this study suggests that, although consumption of EWH can induce changes in gut microbiota composition, it may have difficulty elucidating the direct link between changes in gut microbiota composition and its effects on metabolism and health (Requena et al., 2017).

Table 3. Human and animal studies assessing the effect of eggs consumption on the composition of the gut microbiota

Citation	Study design	Intervention	Trial duration	Participants	Effect on the gut microbiota	Other health or physiological observations
Thomas et al. (2022)	Randomized, controlled cross-over	3 eggs/d (4 wk) choline bitartrate (CB) supplement/d (4 wk)	13 wk	23 Men and women classified with metabolic syndrome (MetS) (35–70 yr old)	Phylum *Firmicutes/ Bacteroidetes* - Shannon -	Not applicable (NA)
Liu et al. (2022a)	Prospective nonrandomized	2 eggs/d (90–100 g, 460–500 mg cholesterol)	2 wk	9 Healthy males [29±1 yr old, body mass index (BMI) 22±1 kg/m^2]	Phylum *Firmicutes/ Bacteroidetes* - Shannon - Simpson - Chao1 -	NA
Zhu et al. (2020)	Randomized, cross-over	2 whole eggs (100 g)/d (4 wk) yolk-free eggs (100 g)/d (4 wk)	12 wk	20 Overweight/obese postmenopausal women [57.7 (±5.64) yr old, average BMI of 28.34 (±2.96)]	Genus *Prevotella* - *Anaeroplasma* - *Clostridium* - *Peptostreptococcaceae* -	NA
Citation	**Control treatment**	**Experimental treatment**	**Feeding duration**	**Body weight**	**Animal model**	**Effect on the gut microbiota**
Avirineni et al. (2022)	Control diet (CON; 4.63 kcal/g)	Egg albumen+cellulose (EC; 4.38 kcal/g) Egg albumen+inulin (EI; 4.63 kcal/g) Whey protein isolate+cellulose (WC; 4.38 kcal/g) Whey protein isolate+inulin (WI; 4.63 kcal/g)	9 wk	442.2±28 g	40 Male obesity-prone Sprague-Dawley rats (3 wk old)	NA
Ge et al. (2021)	Dextran sodium sulfate (DSS)	DSS+egg white peptide (50 mg) DSS+egg white peptide (100 mg) DSS+egg white peptide (200 mg)	2 wk	20.00±2 g	Male BALB/c mice (SPF level)	Phylum *Firmicutes/Bacteroidetes* ↑ Genus *Lactobacillus* ↑ no rank_*f_Ruminococcaceae* ↓ *Ruminiclostridium* ↓ *Candidatus_Saccharimonas* ↑
Zhang et al. (2020)	Distilled water	Egg ovotransferrin (OVT) (≈400 mg)	3 wk control, 3 wk OVT, 8 wk control, and 8 wk OVT	NA	Male C57BL/6J mice (young: 3 wk old) (adult: 8 wk old)	Phylum *Actinobacteria* ↓ (Young) *Actinobacteria* ↑ (Adult) *Proteobacteria* ↑ (Young) TM7 ↓ (Adult) Genus *Akkermansia* ↑ (Young, Adult) Shannon - (Young, Adult)

Table 3. Human and animal studies assessing the effect of eggs consumption on the composition of the gut microbiota (continued)

Citation	Control treatment	Experimental treatment	Feeding duration	Body weight	Animal model	Effect on the gut microbiota
Requena et al. (2017)	Tap water	Egg white hydrolyzed with pepsin	12 wk	250–275 g [Zucker fatty (fa/fa) rats] 150–175 g [Zucker lean (+/+) rats]	20 Male Zucker fatty (fa/fa) rats (8 wk old) 10 Male Zucker lean (+/+) rats (8 wk old)	Phylum *Bacteroides* ↓ Genus *Lactobacillus* / *Enterococcus* ↓ *Bifidobacterium* ↓ Species *Clostridium leptum* ↓
Yu et al. (2020)	Casein	Hen egg white ('HEW' group); duck egg white ('DEW' group); preserved egg white ('PEW' group)	8 wk	(117 g±10 g)	40 Male Sprague–Dawley rats	Phylum *Firmicutes*/*Bacteroidetes* - *Proteobacteria* (DEW ↑) *Verrucomicrobia* (HEW ↑) Family *Peptostreptococcaceae*, *Moraxellase* (DEW ↑) *Lactobacillaceae*, *Lachnospiraceae* (DEW ↓) Genus *Akkermansia* (HEW ↑) Shannon (HEW ↑) Simpson (HEW ↑) Ace (PEW ↓) Chao 1 (PEW ↓)
Meng et al. (2020)	Fresh duck eggs	Preserved duck eggs	8 wk	110–130 g	24 Male Sprague–Dawley rats	Phylum *Firmicutes* - *Bacteroidetes* - *Firmicutes*/*Bacteroidetes* ↓ *Proteobacteria* - Genus *Ruminococcaceae* UCG-005 ↓ *Allobaculum* ↓ *Christensenellaceae* R-7 group ↓ unclassified *Clostridiales* ↓ *Eubacterium ruminantium* group ↑ *Eubacterium xylanophilum* group ↑ *Ruminococcaceae* UCG-009 ↑ *Eubacterium ventriosum* ↑ *Tyzzerella* ↑ Shannon ↑ Simpson ↓

Table 3. Human and animal studies assessing the effect of eggs consumption on the composition of the gut microbiota (continued)

Citation	Control treatment	Experimental treatment	Feeding duration	Body weight	Animal model	Effect on the gut microbiota
Fukunaga et al. (2020)	Casein-beef tallow-based diet	Casein-egg yolk-based diet	14 d	35.0±0.4 g 35.1±0.6 g	16 Male Kwl:ddY mice 5 wk old	Phylum *Firmicutes* ↓ *Epsilonbacteraeota* ↓ Family *Lachnospiraceae* ↓ *Ruminococcaceae* ↓ *Erysipelotrichaceae* ↑ Genus *Parasutterella* ↑ *coprostanoligenes* ↑ Operational taxanomic unit (OTU) ↓ Shannon ↓ Simpson -

Unlike consuming only eggs compared to consuming eggs with prebiotic fiber together, the results of cecal microbiota were changed in 111 species' abundance. The abundances of *Actinobacteria*, *Deinococcus-Thermus*, *Deferribacteres*, and *Verrucomicrobia* were relatively higher than that of the control, and the abundance of *Firmicutes* species was relatively less than that of the control group. These changes in bacterial composition are correlated with the production of plasma metabolites, such as plasma butyric acid, propionic acid, and other metabolites derived from carbohydrate, protein, and fat metabolism, in an obese male rat model (Avirineni et al., 2022).

Choline contained in eggs can produce TMA by enzyme reaction of intestinal microbes, and TMA can be converted into harmful substances which may trigger metabolic diseases such as TMAO (Salzano et al., 2022). In patients with metabolic syndrome, intestinal microbiota and their correlation to metabolites were the subject of a study on the impact of egg consumption. It was found that there was no significant effect on microbial diversity or abundance of taxa (Thomas et al., 2022). Phosphatidylcholine and choline bitartrate are two different forms of choline. Phosphatidylcholine is a type of choline derived from soybean and egg yolk. Choline bitartrate is a type of choline produced through chemical synthesis (Smolders et al., 2019). There was no significant difference between the baseline group, the group with phosphatidylcholine provided by eggs, and the group with choline bitartrate supplement. There was no significant correlation in the correlation analysis between intestinal microflora and TMAO. These results suggest that choline supplied from eggs may not be a major influencer on TMAO production (Thomas et al., 2022).

Whole egg consumption increased plasma choline and betaine in overweight postmenopausal women with mild hypercholesterolemia; however, it did not increase plasma TMAO or alter gut microbiota composition, such as *Prevotella*, *Anaeroplasma*, *Clostridium*, and *Peptostreptococcaceae*, which are associated with TMAO concentrations (Zhu et al., 2020). In addition, whole egg consumption is believed to cause an increase in cholesterol and thereby induce cardiovascular disease. However, consuming two eggs daily for 2 weeks without changing their usual diet in people at low risk of developing metabolic diseases did not cause any changes in the gut microbiota. However, it rather positively modulated the functions of the gut microbiota, improving vascular health and intestinal function (Liu et al., 2022a).

Egg protein

Egg protein refers to the protein found in eggs, which is a complete protein containing all essential amino acids needed by the human body (Puglisi and Fernandez, 2022). One of the egg protein-derived peptides, Isoleucine-Arginine-Tryptophan (lle-Arg-Trp; IRW) and Isoleucine-Glutamine-Tryptophan (lle-Gln-Trp; IQW), reduce tumor necrosis factor (TNF)-induced inflammatory responses and oxidative stress in endothelial cells (Majumder et al., 2013). In one study, consumption of the egg protein transferrin-derived peptides IRW and IQW increased the ACE and Shannon index but decreased the Simpson index in obese mice induced by a high-fat diet. In addition, administration of IRW and IQW reduced the relative abundances of *Firmicutes* and *Parabacteroides*, and IRW increased the abundance of *Bacteroides*, known as the major microorganisms that exhibit anti-obesity effects in the intestine. This study showed that ingesting egg protein-derived peptides alleviates high-fat diet-induced obesity by reprogramming the gut microbiome (Liu et al., 2022b).

Egg yolks and egg whites have different nutritional compositions. Compared to egg yolk, egg white has a relatively low percentage of fat and proteins. In a dextran sulfate sodium (DSS)-induced colitis mouse model study, 200 mg/kg bw of egg white peptide ingestion decreased *Ruminiclostridium* and significantly increased *Lactobacillus* and *Candidatus_Saccharimonas* in the gut microbiome compared to the DSS group. In the correlation analysis, *Lactobacillus* and *Candidatus_Saccharimonas* significantly reduced pro-inflammatory cytokines such as interleukin (IL)-1β and TNF-α. This indicates that the ingestion of egg white peptides can alleviate colonic inflammation by increasing the relative abundance of beneficial bacteria and reducing pro-inflammatory cytokines (Ge et al., 2021). Ovotransferrin (OVT) is an egg white protein well known to have a wide range of biological activities, such as anti-inflammatory, antioxidant, and immunomodulatory functions (Lee et al., 2021). In a clinical study, a diet with OVT positively affected gut health by increasing the proportion of *Akkermansia*, which promotes host immune regulation and intestinal epithelial cell integrity at the genus level of the gut microbiota (Zhang et al., 2020).

Conversely, in a study comparing the cecum microbiota of rats ingesting soy, milk, meat, fish, and egg proteins, along with oligosaccharides, *Erysipelotrichaceae*, *Ruminococcaceae*, and *Lachnospiraceae* were the most abundant families in egg protein and cellulose-fed rats. *Erysipelotrichaceae*, *Bifidobacteriaceae*, and *Lachnospiraceae* were the most abundant families in egg protein and raffinose-fed rats, respectively (Sivixay et al., 2021). *Erysipelotrichaceae*, which was most abundantly increased through the consumption of egg protein and prebiotics, is a characteristic bacterium that is decreased in patients with atopic dermatitis and increased in patients with remission of the disease. For example, *Erysipelatrichaceae_* UCG-003 is a potential probiotic used in a probiotic formula along with other beneficial bacteria and prebiotics (Wang et al., 2022). These results indicate that the growth of *Erysipelotrichaceae*, which can have a positive effect on atopic dermatitis, can be promoted by egg protein (Sivixay et al., 2021).

Conclusion

Previous studies have indicated that the consumption of animal products can affect the gut microbiome, with protein being a key nutritional characteristic of these products. The ingestion of red or processed meat is associated with alterations in the abundance of intestinal *Lachnospiraceae*, although the mechanism of the changes is uncertain. In contrast, white meat protein, such as chicken, is associated with an increased level of *Lactobacillus* in the gut. Consumption of dairy products results in an increase in both *Lactobacillus* and *Bifidobacterium* abundances, and moderate intake of casein and whey protein is associated with elevated levels of LAB. Egg yolk or egg protein can also impact the growth of *Erysipelotrichaceae*.

Although the available scientific evidence is insufficient to confirm a correlation between animal products or their protein and the gut microbiome, current accumulating reports and results point to a relatively consistent direction of future research. Taken together, the present review investigates the effects of these animal products and their protein on the composition of the gut microbiome to enhance our understanding of the metabolism and function of intestinal microorganisms.

Conflicts of Interest

The authors declare no potential conflicts of interest.

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Ethics Approval

This article does not require IRB/IACUC approval because there are no human and animal participants.

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